MULTIMEDIA UNIVERSITY®

STUDENT ID NO

MULTIMEDIA UNIVERSITY

FINAL EXAMINATION

TRIMESTER 1, 2015/2016

HPB2011 – BIOINFORMATICS PROGRAMMING I

(All sections / Groups)

12 OCT 2015
9.00 a.m. – 11.00 a.m.
(2 Hours)

INSTRUCTIONS TO STUDENTS

1. This question paper consists of 6 pages including cover page and 5 questions only.
2. Attempt **FOUR** out of **FIVE** questions. All questions carry equal marks (10), and the distribution of the marks for each question is given.
3. Please write all your answers in the Answer Booklet provided.

QUESTION 1 [10 marks]

a) Explain DOT matrix method in sequence alignment? What are the parameters uses for filtering technique in DOT matrix? **[4 marks]**

b) Construct the Global alignment scoring matrix for given TWO sequences as below:
Seq 1 = AAGCCT
Seq 2 = GCCTT
Match = +2, Mismatch= -1, Gap= -2

Perform the trace-back steps in order to get an optimal alignment. **[4 marks]**

c) What is the central dogma of molecular biology? List down 2 Protein databases available for public? **[2 marks]**

Continue....

QUESTION 2 [10 marks]

a) Briefly explain the differences between sequence similarity and sequence homology?

[3 marks]

b) Briefly explain Biological databases. What are the differences between Primary and Derivative databases?

[4 marks]

c) Briefly explain the different types of protein structure? What are the method used for secondary structure prediction?

[3 marks]

Continue....

QUESTION 3 [10 marks]

a) Write a Java program to define a class of "Sequence". A Sequence may be a gene or a protein. The attributes of a Sequence object must include at least

- an ID
- whether it is a gene or protein
- the source species
- the discoverer
- the sequence itself

Write the class data member declarations. Use appropriate types. **[2 marks]**

b) Your class should have a Constructor which allows to create a Sequence object and initiate the attributes to input values. **[2 marks]**

c) It must also include a "public int match(...)" method to match 2 sequences of the same type (both genes or both proteins). Write the signature of this method, including a correct input parameter. Inside the method check that the type of input is the same as the type of "this" object (i.e. both genes or both proteins), and return a negative number if they are un-equal. Else loop through the elements of both sequences (up to the end of whichever sequence is shorter). If the elements at a position in both sequences match, add 2 to the score, else subtract 1 from the score. Return the final score. **[4 marks]**

d) Explain what an 'exception' is and list 2 different types of exception. **[2 marks]**

Continue....

QUESTION 4 [10 marks]

a) Determine the output of the following code: **[2 marks]**

```
class A{
static int p = 10;
private int q;
A(int x) {
p = p++;
q = x;
System.out.println("q = "+q);
}}
class B extends A {
B(int x, int y){
super(x);
p = y;
}
Public static void main(String[] a) {
A XY = new A(5);
B YY = new B(6 , 7);
System.out.println("p = " + B.p);
}}
```

b) Write a function "countLetters()" which calculates the number of (A,T,C,G) bases in a data member sequence called "DNASeq". This function returns an array containing the number of 4 bases in the sequence. This function should also handle the exception of illegal input in case it finds any letter than 'ATCG' in DNA. **[5 marks]**

c) What is an "Interface"? Declare an interface called "Payable" which consists of howToPay() with integer return and whereToPay() with String return **[3 marks]**

Continue....

QUESTION 5 [10 marks]

a) Define a function *reverse_complement(seq)* that finds the reverse complement of input sequence *seq*. The function gets a sequence through a parameter and returns the reverse complement of the sequence. **[3 marks]**

Hint:

- *complement_map = {'c': 'g', 'g': 'c', 'a': 't', 't': 'a'}*
- *example seq=aaaccc; output=gggttt*

b) Write a function called isPalindrome(String word) which gets and examines whether variable 'word' is palindrome. **[3 marks]**

Hint:

A palindrome is a word, phrase, number, or other sequence of characters which reads the same backward or forward. Such as "racecar"... .

c) Explain the following terms in Object-oriented programming:
Encapsulation, Abstraction, Inheritance, Polymorphism **[4 marks]**

End of paper